

A Simulative Model for the Analysis of Conduction Properties of Ion Channels Based on First-Principle Approaches

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Outline



- The problem and our goal
- State of the art
- Our model and simulative procedure
- Results
- Further research developments

Ideas and hints also from:

M. Cascella, M. Ferrario, J. Kona, S. Moroni, L. Reggiani, B. Roux, V. Torre

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The problem...





VMD snapshot

- Ion channels are nanometric macromolecular pores in cell membranes formed by proteins
- They have selective ion conduction and the ability to gate-open in response to an appropriate stimulus
- Since 1998 X-ray crystallographic structures, provinding atomic resolution of some channel proteins, have been obtained
- KcsA potassium channel is a good prototype to test any realistic simulative model

... and our goal







State of the art



Experimental scenario

Electrical characterization of single open channels embedded in planar lipid bilayers in presence of buffered solutions with symmetrical K+ concentration

(see Miller – USA, Schrempf – Germany)

Theoretical models

- ✓ Single-file multi-ion models (e.g. Hille) (since 1970)
- ✓ Continuum Models, e.g. Poisson-Nernst-Planck (PNP) models (e.g. Heisenberg) (since 1970)
- ✓ Atomistic MD simulations and Brownian-Dynamics simulations (e.g. Roux) (since 1988)

Our simulative procedure...



The possible configurations of the channel are defined through the K+ occupancy of a set of individual binding sites within the pore $(S_{ext}, S_0...S_4, S_{cav})$, identified from structural data and MD simulations, under the hypothesis of single-file concerted motion



The transition rates can be estimated by calculating the average time a given transition needs to take place from MD or using the Kramers' formula:



where the diffusion coefficient D, the energy barrier E_b and the frequency ω_1, ω_2 come directly from MD simulations

Our simulative procedure... 27



The MD approach includes a modified GROMOS87 force-field. The highresolution (2.0 Å) KcsA protein structure is embedded into a wateroctane-water bilayer. A total of 34434 atoms have been considered.

The free-energy difference between the initial and final configurations is evaluated from MD through a multiple-steering dynamics procedure

The ion capture probability assumes an energy barrier of 8 k_BT (approx. 5 Kcal/mol) both at intracellular and extracellular reservoirs and has been estimated from the classical kinetic theory of gases:

$$k_{\text{entry}} = \frac{n\sigma}{6} \sqrt{\frac{k_B T}{2M}} e^{-\frac{E_{in}}{kT}}$$

Being *n* the ion concentration and σ the cross sectional area of the vestibule

Results



Observed transitions



VMD movie

 $(S_{ext}, S_1, S_3, S_{cav}) \rightarrow (S_1, S_3, S_{cav}) \rightarrow (S_1, S_3, S_4) \qquad (S_2, S_4, S_{cav}) \rightarrow (S_1, S_3, S_{cav}) \rightarrow (S_0, S_3, S_{cav})$







Results



Free-energy profile determination



VMD movie

 $(S_1, S_3) \rightarrow (S_2, S_4)$







Experimental data from LeMasurier et al., J. Gen. Physiol., 118 (3), 303 (2001)



Results



Noise Power Spectrum





- ✓ Free-energy mapping for all the relevant conduction paths
- ✓ Analysis of noise to identify possible correlations in ion exit
- ✓ Analysis of conduction properties in presence of gating
- Analysis of permeation properties of several group I ions (K, Na, Rb, ...)
- Analysis of other ion channels, with available structural conformation